OIPE

RAW SEQUENCE LISTING   DATE: 01/27/2002
PATENT APPLICATION: US/10/041,859   TIME: 15:30:42

Input Set : A:\087102us.app
Output Set: N:\CRF3\01272002\J041859.raw

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      3 <110> APPLICANT: HUANG, QIHONG
      4        REED, JOHN C.
      5        DEVERAUX, QUINN L.
      6        MAEDA, SUSUMU
      8 <120> TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
      9        METHODS FOR MAKING AND USING THEM
     11 <130> FILE REFERENCE: 087102/027 2537
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/041,859
C--> 14 <141> CURRENT FILING DATE: 2002-01-07
     16 <150> PRIOR APPLICATION NUMBER: 60/260,478
     17 <151> PRIOR FILING DATE: 2001-01-08
     19 <160> NUMBER OF SEQ ID NOS: 25
     21 <170> SOFTWARE: PatentIn Ver. 2.1
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 3773
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Bombyx mori
     28 <220> FEATURE:
     29 <221> NAME/KEY: CDS
     30 <222> LOCATION: (2733)..(3770)
     32 <400> SEQUENCE: 1
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     37 ttcttgcaag acgagtgtca gtgattaaac aaaaacataa gaatagacgt tttatgcgtt 180
     39 actaaaaaaa aggaaaaata taccaatgga gttgacgaaa gttgctaaaa atggagctgc 240
     41 cgccacgttg gtgatgttaa aaaatgcgcg ggatgcaaaa atgcgacctt tcattggtcc 300
     43 gctcatgtta tcctcgtgtg agtcttcaac gacatccaca ctcccgtcac cttcgtcgtc 360
     45 agctgataaa acggataatc acgacacatt caacttcctt cctgatatgc ccgacatgcg 420
     47 tcgtgaagag gaacgtctga aaacatttga tcagtggccc gttacgtttt tgacgccgga 480
     49 acaattggcc cgcaacggat tctactacct cggtcgcggc gacgaagtgt gctgtgcttt 540
     51 ctgtaaggta gaaattatga ggtgggtcga aggcgacgat cctgccgccg atcatcggag 600
     53 atgggcgccc cagtgtccct ttgtacgaaa acaaatgtat gccaacgctg ggggagaggc 660
     55 gaccgctgtc ggtagagacg aatgtggggc cagtgcggcc acgcagcctc cccgcatgcc 720
     57 cggccccgtg cacgcgcggt actccaccga ggccgcgcgg ctcgccacct tcaaggactg 780
     59 gccgagacgt atgcgccaaa aacccgagga actggcagag gccggattct tctatacagg 840
     61 ccaaggtgac aaaacgaaat gcttctattg cgacggaggg ctaaaagatt gggaaagcga 900
     63 tgacgttccg tgggaacagc acgccagatg gttcgaccgc tgcgcgtacg tgcaattggt 960
     65 gaaaggacgt gactacattc agaaggtgaa gtcggaggcc actgcgatat ctgctagcga 1020
     67 agaagaacag gccgccacca atgattcgac taagaacgtc gcccaagagg gcgagaaaca 1080
     69 tttggatgac tctaaaatat gtaaaatatg ttattccgag gagcgtaacg tgtgcttcgt 1140
     71 gccgtgcggc cacgtggtgg cgtgcgccaa gtgcgcgctg tcgacggaca agtgcccgat 1200
     73 gtgtcgcagg acgttcacga atgcggtgcg gctctacttc tcgtgaaagg accctcctcg 1260
     75 cgagctgtat actaatcact tcaccgggcg gccctggagc gtgctgaaac caccccttcga 1320
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 77 acgaaaccgc gtatcctgtg attttttacat taaataaatt tacaaattga tagcggtggg 1380
 79 gcaatgtata ggaactcgtc agaactcgcg agttgacgtg caggaaggag ttagtgattt 1440
 81 gtaaacttgt aaactgatgt tgaaatgatt ttatttatta tttaaaattc taatgacaaa 1500
 83 gtgtaagtaa ataaatgtac atattatttt agattatcag tttgtcccac cgacaaaagt 1560
 85 gaaatgtaca taggtgtttt catatcactt caacagtcga agaccttctt tttgaattta 1620
 87 aggatatata tttatacata taaattaaaa ttttaacgag acatcaatat aaatggttta 1680
 89 acaacttatt tatacactga aatcaagtga agtgtaacat ggtctgaaga atgtttttact 1740
 91 gatttcactt cccctgttga agtgataaaa ttctaatgta aatccagagt ttaaatgtcg 1800
 93 tcataattaa tataagaaac aagtttttacg cttcttttgc ttgaaaaatc ttataattga 1860
 95 ttcaggaatt atttaatgtg actatatttt gttcctgtaa ataacataat atatactatt 1920
 97 tattgattaa ttctgacata atttatggca attccgtaag atacaatcca atacttatttt 1980
 99 catgtaactc acttcaaaat agttgaatgt gtggtgtgat tataatgtta aatgtctaaa 2040
101 tttataataa attgagcaaa gttgcattta atgtatgaat actaattatt gtttttaacaa 2100
103 aacatttaag tataatctgc tctgtgatttt taatgtatca agaaataacc ccaacacctt 2160
105 aattgaagtt tttacattgt tgctgataaa aaaaatcata tcaattacat ttacaagtca 2220
107 atttttaattg ttcagaaacc aaacacaatt ttgttagtga ctcctgcttt acgaagtagt 2280
109 atgacaaacc agtgtttcgt tgattgcatt aatttagttg taaccaatat ttacactcaa 2340
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113 aatacaatcc cgcacaagcc atttgcaagt ttctacacaa ctaaaacgta ttgtatccat 2460
115 tatctatacg tcatatcatt aatatatact tgctttagca aacatatatt cacgaataac 2520
117 ttcacaatat atttttgtaa atcaacatat taatggtaat taacgaatcg cacggtacaa 2580
119 atagtgataa ctgctgagtg cactaaatag taagagaatt tatttaaaca gtcaaatttt 2640
121 gtttcataag tagttattttc atactgttga atgttattca ttaaaacaaa tgttaaagca 2700
123 aaaaaaaaaa aaaaagtcg tgactgggaa aa atg gag ttg acg aaa gtt gct 2753
124                                     Met Glu Leu Thr Lys Val Ala
125                                      1               5
127 aaa aat gga gct gcc gcc acg ttg gtg atg tta aaa aat gcg cgg gat 2801
128 Lys Asn Gly Ala Ala Ala Thr Leu Val Met Leu Lys Asn Ala Arg Asp
129           10              15              20
131 gca aaa atg cga cct ttc att ggt ccg ctc atg tta tcc tcg tgt gag 2849
132 Ala Lys Met Arg Pro Phe Ile Gly Pro Leu Met Leu Ser Ser Cys Glu
133      25              30              35
135 tct tca acg aca tcc aca ctc ccg tca cct tcg tcg tca gct gat aaa 2897
136 Ser Ser Thr Thr Ser Thr Leu Pro Ser Pro Ser Ser Ser Ala Asp Lys
137  40              45              50                      55
139 acg gat aat cac gac aca ttc aac ttc ctt cct gat atg ccc gac atg 2945
140 Thr Asp Asn His Asp Thr Phe Asn Phe Leu Pro Asp Met Pro Asp Met
141              60              65              70
143 cgt cgt gaa gag gaa cgt ctg aaa aca ttt gat cag tgg ccc gtt acg 2993
144 Arg Arg Glu Glu Glu Arg Leu Lys Thr Phe Asp Gln Trp Pro Val Thr
145          75              80              85
147 ttt ttg acg ccg gaa caa ttg gcc cgc aac gga ttc tac tac ctc ggt 3041
148 Phe Leu Thr Pro Glu Gln Leu Ala Arg Asn Gly Phe Tyr Tyr Leu Gly
149          90              95              100
151 cgc ggc gac gaa gtg tgc tgt gct ttc tgt aag gta gaa att atg agg 3089
152 Arg Gly Asp Glu Val Cys Cys Ala Phe Cys Lys Val Glu Ile Met Arg
153      105             110             115
155 tgg gtc gaa ggc gac gat cct gcc gcc gat cat cgg aga tgg gcg ccc 3137
156 Trp Val Glu Gly Asp Asp Pro Ala Ala Asp His Arg Arg Trp Ala Pro
```

```
157 120                     125                 130                 135
159 cag tgt ccc ttt gta cga aaa caa atg tat gcc aac gct ggg gga gag   3185
160 Gln Cys Pro Phe Val Arg Lys Gln Met Tyr Ala Asn Ala Gly Gly Glu
161                     140                 145                 150
163 gcg acc gct gtc ggt aga gac gaa tgt ggg gcc agt gcg gcc acg cag   3233
164 Ala Thr Ala Val Gly Arg Asp Glu Cys Gly Ala Ser Ala Ala Thr Gln
165                     155                 160                 165
167 cct ccc cgc atg ccc ggc ccc gtg cac gcg cgg tac tcc acc gag gcc   3281
168 Pro Pro Arg Met Pro Gly Pro Val His Ala Arg Tyr Ser Thr Glu Ala
169                 170                 175                 180
171 gcg cgg ctc gcc acc ttc aag gac tgg ccg aga cgt atg cgc caa aaa   3329
172 Ala Arg Leu Ala Thr Phe Lys Asp Trp Pro Arg Arg Met Arg Gln Lys
173         185                 190                 195
175 ccc gag gaa ctg gca gag gcc gga ttc ttc tat aca ggc caa ggt gac   3377
176 Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln Gly Asp
177 200                 205                 210                 215
179 aaa acg aaa tgc ttc tat tgc gac gga ggg cta aaa gat tgg gaa agc   3425
180 Lys Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Ser
181                     220                 225                 230
183 gat gac gtt ccg tgg gaa cag cac gcc aga tgg ttc gac cgc tgc gcg   3473
184 Asp Asp Val Pro Trp Glu Gln His Ala Arg Trp Phe Asp Arg Cys Ala
185                 235                 240                 245
187 tac gtg caa ttg gtg aaa gga cgt gac tac att cag aag gtg aag tcg   3521
188 Tyr Val Gln Leu Val Lys Gly Arg Asp Tyr Ile Gln Lys Val Lys Ser
189         250                 255                 260
191 gag gcc act gcg ata tct gct agc gaa gaa gaa cag gcc gcc acc aat   3569
192 Glu Ala Thr Ala Ile Ser Ala Ser Glu Glu Glu Gln Ala Ala Thr Asn
193         265                 270                 275
195 gat tcg act aag aac gtc gcc caa gag ggc gag aaa cat ttg gat gac   3617
196 Asp Ser Thr Lys Asn Val Ala Gln Glu Gly Glu Lys His Leu Asp Asp
197 280                 285                 290                 295
199 tct aaa ata tgt aaa ata tgt tat tcc gag gag cgt aac gtg tgc ttc   3665
200 Ser Lys Ile Cys Lys Ile Cys Tyr Ser Glu Glu Arg Asn Val Cys Phe
201                 300                 305                 310
203 gtg ccg tgc ggc cac gtg gtg gcg tgc gcc aag tgc gcg ctg tcg acg   3713
204 Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Thr
205             315                 320                 325
207 gac aag tgc ccg atg tgt cgc agg acg ttc acg aat gcg gtg cgg ctc   3761
208 Asp Lys Cys Pro Met Cys Arg Arg Thr Phe Thr Asn Ala Val Arg Leu
209         330                 335                 340
211 tac ttc tcg tga                                                   3773
212 Tyr Phe Ser
213     345
216 <210> SEQ ID NO: 2
217 <211> LENGTH: 346
218 <212> TYPE: PRT
219 <213> ORGANISM: Bombyx mori
221 <400> SEQUENCE: 2
222 Met Glu Leu Thr Lys Val Ala Lys Asn Gly Ala Ala Ala Thr Leu Val
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```
223   1               5               10              15
225 Met Leu Lys Asn Ala Arg Asp Ala Lys Met Arg Pro Phe Ile Gly Pro
226             20              25              30
228 Leu Met Leu Ser Ser Cys Glu Ser Ser Thr Thr Ser Thr Leu Pro Ser
229         35              40              45
231 Pro Ser Ser Ser Ala Asp Lys Thr Asp Asn His Asp Thr Phe Asn Phe
232     50              55              60
234 Leu Pro Asp Met Pro Asp Met Arg Arg Glu Glu Glu Arg Leu Lys Thr
235  65              70              75              80
237 Phe Asp Gln Trp Pro Val Thr Phe Leu Thr Pro Glu Gln Leu Ala Arg
238             85              90              95
240 Asn Gly Phe Tyr Tyr Leu Gly Arg Gly Asp Glu Val Cys Cys Ala Phe
241         100             105             110
243 Cys Lys Val Glu Ile Met Arg Trp Val Glu Gly Asp Asp Pro Ala Ala
244         115             120             125
246 Asp His Arg Arg Trp Ala Pro Gln Cys Pro Phe Val Arg Lys Gln Met
247     130             135             140
249 Tyr Ala Asn Ala Gly Gly Glu Ala Thr Ala Val Gly Arg Asp Glu Cys
250 145             150             155             160
252 Gly Ala Ser Ala Ala Thr Gln Pro Pro Arg Met Pro Gly Pro Val His
253             165             170             175
255 Ala Arg Tyr Ser Thr Glu Ala Ala Arg Leu Ala Thr Phe Lys Asp Trp
256         180             185             190
258 Pro Arg Arg Met Arg Gln Lys Pro Glu Glu Leu Ala Glu Ala Gly Phe
259         195             200             205
261 Phe Tyr Thr Gly Gln Gly Asp Lys Thr Lys Cys Phe Tyr Cys Asp Gly
262     210             215             220
264 Gly Leu Lys Asp Trp Glu Ser Asp Asp Val Pro Trp Glu Gln His Ala
265 225             230             235             240
267 Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln Leu Val Lys Gly Arg Asp
268             245             250             255
270 Tyr Ile Gln Lys Val Lys Ser Glu Ala Thr Ala Ile Ser Ala Ser Glu
271         260             265             270
273 Glu Glu Gln Ala Ala Thr Asn Asp Ser Thr Lys Asn Val Ala Gln Glu
274         275             280             285
276 Gly Glu Lys His Leu Asp Asp Ser Lys Ile Cys Lys Ile Cys Tyr Ser
277     290             295             300
279 Glu Glu Arg Asn Val Cys Phe Val Pro Cys Gly His Val Val Ala Cys
280 305             310             315             320
282 Ala Lys Cys Ala Leu Ser Thr Asp Lys Cys Pro Met Cys Arg Arg Thr
283         325             330             335
285 Phe Thr Asn Ala Val Arg Leu Tyr Phe Ser
286         340             345
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289 <210> SEQ ID NO: 3
290 <211> LENGTH: 20
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

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```
297 <220> FEATURE:
298 <221> NAME/KEY: modified_base
299 <222> LOCATION: (3)
300 <223> OTHER INFORMATION: a, c, g or t
302 <220> FEATURE:
303 <221> NAME/KEY: modified_base
304 <222> LOCATION: (6)
305 <223> OTHER INFORMATION: a, c, g or t
307 <220> FEATURE:
308 <221> NAME/KEY: modified_base
309 <222> LOCATION: (9)
310 <223> OTHER INFORMATION: a, c, g or t
312 <220> FEATURE:
313 <221> NAME/KEY: modified_base
314 <222> LOCATION: (12)
315 <223> OTHER INFORMATION: a, c, g or t
317 <400> SEQUENCE: 3
318 gcngangcng gnttyttyta                                            20
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 17
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
329 <220> FEATURE:
330 <221> NAME/KEY: modified_base
331 <222> LOCATION: (3)
332 <223> OTHER INFORMATION: a, c, g or t
334 <220> FEATURE:
335 <221> NAME/KEY: modified_base
336 <222> LOCATION: (9)
337 <223> OTHER INFORMATION: a, c, g or t
339 <220> FEATURE:
340 <221> NAME/KEY: modified_base
341 <222> LOCATION: (15)
342 <223> OTHER INFORMATION: a, c, g or t
344 <400> SEQUENCE: 4
345 acnacrtgnc crcangg                                               17
348 <210> SEQ ID NO: 5
349 <211> LENGTH: 18
350 <212> TYPE: DNA
351 <213> ORGANISM: Artificial Sequence
353 <220> FEATURE:
354 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
356 <400> SEQUENCE: 5
357 ctgttcccac ggaacgtc                                              18
360 <210> SEQ ID NO: 6
361 <211> LENGTH: 17
362 <212> TYPE: DNA
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/041,859**

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Input Set : **A:\087102us.app**
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```
L:13  M:270 C: Current Application Number differs, Replaced Application Number
L:14  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
```